

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/380,337

DATE: 10/09/2001

TIME: 07:09:19

Input Set : A:\-315-1.app

Output Set: N:\CRF3\10092001\I380337.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Chandrasekharappa, Settara C.

7 Guru, Siradanahalli C.

8 Manickam, Pachiappan

9 Collins, Francis S.

10 Emmert-Buck, Michael R.

11 Debelenko, Larisa V.

12 Lubensky, Irina A.

13 Liotta, Lance A.

14 Agarwal, Sunita K.

15 Spiegel, Allen M.

18 (ii) TITLE OF INVENTION: MEN1, the Gene Associated With Multiple

19 Endocrine Neoplasia Type 1, Menin Polypeptides, and Uses

20 Thereof

22 (iii) NUMBER OF SEQUENCES: 28

24 (iv) CORRESPONDENCE ADDRESS:

25 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

26 (B) STREET: Two Embarcadero Center, Eighth Floor

27 (C) CITY: San Francisco

28 (D) STATE: California

29 (E) COUNTRY: USA

30 (F) ZIP: 94111-3834

32 (v) COMPUTER READABLE FORM:

33 (A) MEDIUM TYPE: Floppy disk

34 (B) COMPUTER: IBM PC compatible

35 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

36 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

38 (vi) CURRENT APPLICATION DATA:

C--&gt; 39 (A) APPLICATION NUMBER: US/09/380,337

C--&gt; 40 (B) FILING DATE: 09-Mar-2000

41 (C) CLASSIFICATION:

47 (vii) PRIOR APPLICATION DATA:

44 (A) APPLICATION NUMBER: US 60/040,269

45 (B) FILING DATE: 05-MAR-1997

48 (A) APPLICATION NUMBER: WO PCT/US98/04258

49 (B) FILING DATE: 04-MAR-1998

51 (viii) ATTORNEY/AGENT INFORMATION:

52 (A) NAME: Lockyer, Jean M.

53 (B) REGISTRATION NUMBER: 44,879

54 (C) REFERENCE/DOCKET NUMBER: 015280-315100US

56 (ix) TELECOMMUNICATION INFORMATION:

57 (A) TELEPHONE: (415) 576-0200

58 (B) TELEFAX: (415) 576-0300

61 (2) INFORMATION FOR SEQ ID NO: 1:

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 2772 base pairs

ENTERED

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65         (B) TYPE: nucleic acid
66         (C) STRANDEDNESS: single
67         (D) TOPOLOGY: linear
69     (ii) MOLECULE TYPE: cDNA
72     (ix) FEATURE:
73         (A) NAME/KEY: CDS
74         (B) LOCATION: 111..1940
75         (D) OTHER INFORMATION: /product= "human menin"
77     (ix) FEATURE:
78         (A) NAME/KEY: exon
79         (B) LOCATION: 1..87
81     (ix) FEATURE:
82         (A) NAME/KEY: exon
83         (B) LOCATION: 88..555
85     (ix) FEATURE:
86         (A) NAME/KEY: exon
87         (B) LOCATION: 556..764
89     (ix) FEATURE:
90         (A) NAME/KEY: exon
91         (B) LOCATION: 765..893
93     (ix) FEATURE:
94         (A) NAME/KEY: exon
95         (B) LOCATION: 894..934
97     (ix) FEATURE:
98         (A) NAME/KEY: exon
99         (B) LOCATION: 935..1022
101    (ix) FEATURE:
102        (A) NAME/KEY: exon
103        (B) LOCATION: 1023..1159
105    (ix) FEATURE:
106        (A) NAME/KEY: exon
107        (B) LOCATION: 1160..1295
109    (ix) FEATURE:
110        (A) NAME/KEY: exon
111        (B) LOCATION: 1296..1460
113    (ix) FEATURE:
114        (A) NAME/KEY: exon
115        (B) LOCATION: 1461..2764
118    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
120 GGTGTCCGGA GCCGCGGACC TAGAGATCCC AGAAGCCACA GCGCAGCGGC CCGGCCCCGCC      60
122 ACTATTTCCTA GGCTCTGCGG GGCAGGGGCC GCCGCCACC GCCCGCCGCC ATG GGG      116
123                                     Met Gly
124                                     1
126 CTG AAG GCC GCC CAG AAG ACG CTG TTC CCG CTG CGC TCC ATC GAC GAC      164
127 Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile Asp Asp
128         5                10                15
130 GTG GTG CGC CTG TTT GCT GCC GAG CTG GGC CGA GAG GAG CCG GAC CTG      212
131 Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro Asp Leu
132     20                25                30

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134	GTG	CTC	CTT	TCC	TTG	GTG	CTG	GGC	TTC	GTG	GAG	CAT	TTT	CTG	GCT	GTC	260
135	Val	Leu	Leu	Ser	Leu	Val	Leu	Gly	Phe	Val	Glu	His	Phe	Leu	Ala	Val	
136	35				40					45						50	
138	AAC	CGC	GTC	ATC	CCT	ACC	AAC	GTT	CCC	GAG	CTC	ACC	TTC	CAG	CCC	AGC	308
139	Asn	Arg	Val	Ile	Pro	Thr	Asn	Val	Pro	Glu	Leu	Thr	Phe	Gln	Pro	Ser	
140					55					60						65	
142	CCC	GCC	CCC	GAC	CCG	CCT	GGC	GGC	CTC	ACC	TAC	TTT	CCC	GTG	GCC	GAC	356
143	Pro	Ala	Pro	Asp	Pro	Pro	Gly	Gly	Leu	Thr	Tyr	Phe	Pro	Val	Ala	Asp	
144				70					75					80			
146	CTG	TCT	ATC	ATC	GCC	GCC	CTC	TAT	GCC	CGC	TTC	ACC	GCC	CAG	ATC	CGA	404
147	Leu	Ser	Ile	Ile	Ala	Ala	Leu	Tyr	Ala	Arg	Phe	Thr	Ala	Gln	Ile	Arg	
148			85					90					95				
150	GGC	GCC	GTC	GAC	CTG	TCC	CTC	TAT	CCT	CGA	GAA	GGG	GGT	GTC	TCC	AGC	452
151	Gly	Ala	Val	Asp	Leu	Ser	Leu	Tyr	Pro	Arg	Glu	Gly	Gly	Val	Ser	Ser	
152	100						105					110					
154	CGT	GAG	CTG	GTG	AAG	AAG	GTC	TCC	GAT	GTC	ATA	TGG	AAC	AGC	CTC	AGC	500
155	Arg	Glu	Leu	Val	Lys	Lys	Val	Ser	Asp	Val	Ile	Trp	Asn	Ser	Leu	Ser	
156	115				120					125						130	
158	CGC	TCC	TAC	TTC	AAG	GAT	CGG	GCC	CAC	ATC	CAG	TCC	CTC	TTC	AGC	TTC	548
159	Arg	Ser	Tyr	Phe	Lys	Asp	Arg	Ala	His	Ile	Gln	Ser	Leu	Phe	Ser	Phe	
160				135					140						145		
162	ATC	ACA	GGC	ACC	AAA	TTG	GAC	AGC	TCC	GGT	GTG	GCC	TTT	GCT	GTG	GTT	596
163	Ile	Thr	Gly	Thr	Lys	Leu	Asp	Ser	Ser	Gly	Val	Ala	Phe	Ala	Val	Val	
164			150					155					160				
166	GGG	GCC	TGC	CAG	GCC	CTG	GGT	CTC	CGG	GAT	GTC	CAC	CTC	GCC	CTG	TCT	644
167	Gly	Ala	Cys	Gln	Ala	Leu	Gly	Leu	Arg	Asp	Val	His	Leu	Ala	Leu	Ser	
168		165					170					175					
170	GAG	GAT	CAT	GCC	TGG	GTA	GTG	TTT	GGG	CCC	AAT	GGG	GAG	CAG	ACA	GCT	692
171	Glu	Asp	His	Ala	Trp	Val	Val	Phe	Gly	Pro	Asn	Gly	Glu	Gln	Thr	Ala	
172		180					185					190					
174	GAG	GTC	ACC	TGG	CAC	GGC	AAG	GGC	AAC	GAG	GAC	CGC	AGG	GGC	CAG	ACA	740
175	Glu	Val	Thr	Trp	His	Gly	Lys	Gly	Asn	Glu	Asp	Arg	Arg	Gly	Gln	Thr	
176	195				200					205						210	
178	GTC	AAT	GCC	GGT	GTG	GCT	GAG	CGG	AGC	TGG	CTG	TAC	CTG	AAA	GGA	TCA	788
179	Val	Asn	Ala	Gly	Val	Ala	Glu	Arg	Ser	Trp	Leu	Tyr	Leu	Lys	Gly	Ser	
180				215						220					225		
182	TAC	ATG	CGC	TGT	GAC	CGC	AAG	ATG	GAG	GTG	GCG	TTC	ATG	GTG	TGT	GCC	836
183	Tyr	Met	Arg	Cys	Asp	Arg	Lys	Met	Glu	Val	Ala	Phe	Met	Val	Cys	Ala	
184			230					235						240			
186	ATC	AAC	CCT	TCC	ATT	GAC	CTG	CAC	ACC	GAC	TCG	CTG	GAG	CTT	CTG	CAG	884
187	Ile	Asn	Pro	Ser	Ile	Asp	Leu	His	Thr	Asp	Ser	Leu	Glu	Leu	Leu	Gln	
188		245					250						255				
190	CTG	CAG	CAG	AAG	CTG	CTC	TGG	CTG	CTC	TAT	GAC	CTG	GGA	CAT	CTG	GAA	932
191	Leu	Gln	Gln	Lys	Leu	Leu	Trp	Leu	Leu	Tyr	Asp	Leu	Gly	His	Leu	Glu	
192		260					265					270					
194	AGG	TAC	CCC	ATG	GCC	TTA	GGG	AAC	CTG	GCA	GAT	CTA	GAG	GAG	CTG	GAG	980
195	Arg	Tyr	Pro	Met	Ala	Leu	Gly	Asn	Leu	Ala	Asp	Leu	Glu	Glu	Leu	Glu	
196	275				280					285						290	
198	CCC	ACC	CCT	GGC	CGG	CCA	GAC	CCA	CTC	ACC	CTC	TAC	CAC	AAG	GGC	ATT	1028

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199	Pro	Thr	Pro	Gly	Arg	Pro	Asp	Pro	Leu	Thr	Leu	Tyr	His	Lys	Gly	Ile	
200					295					300					305		
202	GCC	TCA	GCC	AAG	ACC	TAC	TAT	CGG	GAT	GAA	CAC	ATC	TAC	CCC	TAC	ATG	1076
203	Ala	Ser	Ala	Lys	Thr	Tyr	Tyr	Arg	Asp	Glu	His	Ile	Tyr	Pro	Tyr	Met	
204				310					315					320			
206	TAC	CTG	GCT	GGC	TAC	CAC	TGT	CGC	AAC	CGC	AAT	GTG	CGG	GAA	GCC	CTG	1124
207	Tyr	Leu	Ala	Gly	Tyr	His	Cys	Arg	Asn	Arg	Asn	Val	Arg	Glu	Ala	Leu	
208				325				330					335				
210	CAG	GCC	TGG	GCG	GAC	ACG	GCC	ACT	GTC	ATC	CAG	GAC	TAC	AAC	TAC	TGC	1172
211	Gln	Ala	Trp	Ala	Asp	Thr	Ala	Thr	Val	Ile	Gln	Asp	Tyr	Asn	Tyr	Cys	
212		340					345				350						
214	CGG	GAA	GAC	GAG	GAG	ATC	TAC	AAG	GAG	TTC	TTT	GAA	GTA	GCC	AAT	GAT	1220
215	Arg	Glu	Asp	Glu	Glu	Ile	Tyr	Lys	Glu	Phe	Phe	Glu	Val	Ala	Asn	Asp	
216	355					360				365					370		
218	GTC	ATC	CCC	AAC	CTG	CTG	AAG	GAG	GCA	GCC	AGC	TTG	CTG	GAG	GCG	GGC	1268
219	Val	Ile	Pro	Asn	Leu	Leu	Lys	Glu	Ala	Ala	Ser	Leu	Leu	Glu	Ala	Gly	
220				375					380					385			
222	GAG	GAG	CGG	CCG	GGG	GAG	CAA	AGC	CAG	GGC	ACC	CAG	AGC	CAA	GGT	TCC	1316
223	Glu	Glu	Arg	Pro	Gly	Glu	Gln	Ser	Gln	Gly	Thr	Gln	Ser	Gln	Gly	Ser	
224				390				395					400				
226	GCC	CTC	CAG	GAC	CCT	GAG	TGC	TTC	GCC	CAC	CTG	CTG	CGA	TTC	TAC	GAC	1364
227	Ala	Leu	Gln	Asp	Pro	Glu	Cys	Phe	Ala	His	Leu	Leu	Arg	Phe	Tyr	Asp	
228			405				410					415					
230	GGC	ATC	TGC	AAA	TGG	GAG	GAG	GGC	AGT	CCC	ACG	CCT	GTG	CTG	CAC	GTG	1412
231	Gly	Ile	Cys	Lys	Trp	Glu	Glu	Gly	Ser	Pro	Thr	Pro	Val	Leu	His	Val	
232		420				425				430							
234	GGC	TGG	GCC	ACC	TTT	CTT	GTG	CAG	TCC	CTA	GGC	CGT	TTT	GAG	GGA	CAG	1460
235	Gly	Trp	Ala	Thr	Phe	Leu	Val	Gln	Ser	Leu	Gly	Arg	Phe	Glu	Gly	Gln	
236	435				440				445					450			
238	GTG	CGG	CAG	AAG	GTG	CGC	ATA	GTG	AGC	CGA	GAG	GCC	GAG	GCG	GCC	GAG	1508
239	Val	Arg	Gln	Lys	Val	Arg	Ile	Val	Ser	Arg	Glu	Ala	Glu	Ala	Ala	Glu	
240				455				460					465				
242	GCC	GAG	GAG	CCG	TGG	GGC	GAG	GAA	GCC	CGG	GAA	GGC	CGG	CGG	CGG	GGC	1556
243	Ala	Glu	Glu	Pro	Trp	Gly	Glu	Glu	Ala	Arg	Glu	Gly	Arg	Arg	Arg	Gly	
244			470				475						480				
246	CCA	CGG	CGG	GAG	TCC	AAG	CCA	GAG	GAG	CCC	CCG	CCG	CCC	AAG	AAG	CCA	1604
247	Pro	Arg	Arg	Glu	Ser	Lys	Pro	Glu	Glu	Pro	Pro	Pro	Pro	Lys	Lys	Pro	
248			485				490					495					
250	GCA	CTG	GAC	AAG	GGC	CTG	GGC	ACC	GGC	CAG	GGT	GCA	GTG	TCA	GGA	CCC	1652
251	Ala	Leu	Asp	Lys	Gly	Leu	Gly	Thr	Gly	Gln	Gly	Ala	Val	Ser	Gly	Pro	
252		500				505				510							
254	CCC	CGG	AAG	CCT	CCT	GGG	ACT	GTC	GCT	GGC	ACA	GCC	CGA	GGC	CCT	GAA	1700
255	Pro	Arg	Lys	Pro	Pro	Gly	Thr	Val	Ala	Gly	Thr	Ala	Arg	Gly	Pro	Glu	
256	515				520				525					530			
258	GGT	GGC	AGC	ACG	GCT	CAG	GTG	CCA	GCA	CCC	GCA	GCA	TCA	CCA	CCG	CCG	1748
259	Gly	Gly	Ser	Thr	Ala	Gln	Val	Pro	Ala	Pro	Ala	Ala	Ser	Pro	Pro	Pro	
260				535				540					545				
262	GAG	GGT	CCA	GTG	CTC	ACT	TTC	CAG	AGT	GAG	AAG	ATG	AAG	GGC	ATG	AAG	1796
263	Glu	Gly	Pro	Val	Leu	Thr	Phe	Gln	Ser	Glu	Lys	Met	Lys	Gly	Met	Lys	

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264          550          555          560
266 GAG CTG CTG GTG GCC ACC AAG ATC AAC TCG AGC GCC ATC AAG CTG CAA      1844
267 Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys Leu Gln
268          565          570          575
270 CTC ACG GCA CAG TCG CAA GTG CAG ATG AAG AAG CAG AAA GTG TCC ACC      1892
271 Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val Ser Thr
272          580          585          590
274 CCT AGT GAC TAC ACT CTG TCT TTC CTC AAG CGG CAG CGC AAA GGC CTC      1940
275 Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys Gly Leu
276 595          600          605          610
278 TGA ACTACTG GGGACTTCGG ACCGCTTGTG GGGACCCAGG CTCCGCCTTA GTCCCCCAAC      2000
280 TCTGAGCCCA TGTTCTGCCC CCAGCCCAAA GGGGACAGGC CTCACCTCTA CCCAAACCCCT      2060
282 AGGTTCCTCGG TCCCGAGTAC AGTCTGTATC AAACCCACGA TTTTCTCCAG CTCAGAACCC      2120
284 AGGGCTCTGC CCCAGTCGTT AGAATATAGG TCTCTTCTCC CAGAATCCCA GCCGGCCAAT      2180
286 GGAAACCTCA CGCTGGGTCC TAATTACCAG TCTTTAAAGG CCCAGCCCCT AGAAACCCAA      2240
288 GTCCTCCTC GGAACCGCTC ACCTAGAGCC AGACCAACGT TACTCAGGGC TCCTCCCAGC      2300
290 TTGTAGGAGC TGAGGTTTCA CCCTTAACCC AAGGGAGCAC AGGTCCCACC TCCAGCCCGG      2360
292 GGAGCCTAGG ACCACTCAGC CCCTAGGAGT ATATTTCCGC ACTTCAGAAT TCCATATCTT      2420
294 GCGAATCCAA GCTCCCTGCC CCAAATAACT TCAGTCCTGC TTCCAGAATT TGGAAATCCT      2480
296 AGTTTCCTCT CCTTCGTATC CCGAGTCTGG GACACAAAAC TCCGCCCCCA GCCTATGAGC      2540
298 ATCCTGAGCC CCGCCCTCTT CCTGACGAAA CTGGCCCCCGG ATCAGAGCAG GACCTCCCTT      2600
300 CCGACCTCT GGAACCTCC CAGAGGTCCA GCCCATCTCG GAGCATCCCG GAGGAAATCT      2660
302 GCAGAGGGGT TAGGAGTGGG TGACAAGAGC CTGATCTCTT CCTGTTTTGT ACATAGATTT      2720
304 ATTTTTCAGT TCCAAGAAAG ATGAATACAT TTTGTTAAAA AAAAAAAAAA AA      2772
307 (2) INFORMATION FOR SEQ ID NO: 2:
309     (i) SEQUENCE CHARACTERISTICS:
310         (A) LENGTH: 610 amino acids
311         (B) TYPE: amino acid
312         (D) TOPOLOGY: linear
314     (ii) MOLECULE TYPE: protein
316     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
318 Met Gly Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile
319  1          5          10          15
321 Asp Asp Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro
322          20          25          30
324 Asp Leu Val Leu Leu Ser Leu Val Leu Gly Phe Val Glu His Phe Leu
325          35          40          45
327 Ala Val Asn Arg Val Ile Pro Thr Asn Val Pro Glu Leu Thr Phe Gln
328          50          55          60
330 Pro Ser Pro Ala Pro Asp Pro Pro Gly Gly Leu Thr Tyr Phe Pro Val
331  65          70          75          80
333 Ala Asp Leu Ser Ile Ile Ala Ala Leu Tyr Ala Arg Phe Thr Ala Gln
334          85          90          95
336 Ile Arg Gly Ala Val Asp Leu Ser Leu Tyr Pro Arg Glu Gly Gly Val
337          100          105          110
339 Ser Ser Arg Glu Leu Val Lys Lys Val Ser Asp Val Ile Trp Asn Ser
340          115          120          125
342 Leu Ser Arg Ser Tyr Phe Lys Asp Arg Ala His Ile Gln Ser Leu Phe
343          130          135          140

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## VERIFICATION SUMMARY

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L:39 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:40 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:941 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:957 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:973 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:989 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:1005 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:1021 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13  
L:1037 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
L:1053 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15  
L:1069 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16  
L:1085 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17  
L:1101 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18  
L:1117 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19  
L:1133 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20  
L:1149 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21  
L:1165 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22  
L:1181 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23  
L:1197 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24  
L:1213 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25  
L:1229 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26  
L:1245 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27  
L:1261 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28